




Steven M. Ruben
Appl. No. 10/662,429

Department Molecular Biology
Subject Enzymology
Name Guo, Y. & Yu, Y.
Address 1-1000 7th St. N.
 National Brand 43-648
Computation Notebook
Dennison Stationery Products Co., Framingham, MA 01701

75 Sheets
11 1/4" x 9 1/2"
4x4 Quad.
0 73333 43648 8


BEST AVAILABLE COPY

Ruben EXHIBIT #61

Department Biological Biology
Subject Genetics
Name Guo, J. / Y. II
Address 1-11

 43-648

Computation Notebook
Dennison Stationery Products Co., Framingham, MA 01701

 75 Sheets
11 1/4" x 9 1/4"
4x4 Quad.

0 73333 43648 8

Ruben EXHIBIT 2061
Ruben v. Wiley et al.
Interference No. 105.077
RX 2061

8/21/95 Two New TNF: HPDD012 TNF epsilon
HCTBT71 TNF delta

there are differences between the two clones maybe splice variant

Oligo capture cloned full length Named HCTBT71S09

design oligos for seq Rpo2 CTCCAGCTTGGAAAGACCA
Rpo3 TTCTGCATGCCACACCTCTC
Fpo6 GAACA GAAGC AAGATATCCG

design oligos for δ -specific [intron]?

design oligos for construct into pOE70

TNF δ -SPH1: CGCGCATGCAAGGATCAAGGAGCC

TNF δ -HindIII: CGCAAGCTTACAAATCAAGTTTCAAC

TNF δ -specific oligo is given to L. Xing for Northern

8/28/95 PCR to generate insert DNA for following constructs

1. TNF α SphI + HindIII \rightarrow pOE70

2. TNF β SphI + HindIII \rightarrow pOE70

3. TNF γ d39 NcoI + HindIII \rightarrow pOE60

4. TNF γ FL BamHI + BamHI 3' \rightarrow N346

5. TNF γ FL BamHI + BamHI 3' \rightarrow New CHO vector

10 μ l 10X PCR bf BM-

10 μ l 2mm dNTP- CBB

oligos

0.5 μ l PWO polymerase

100 μ l

95 $^{\circ}$ C 2' 30[95 $^{\circ}$ C 1' 55 $^{\circ}$ C 1' 72 $^{\circ}$ C 1'] 75 $^{\circ}$ C 5 min

PCR \rightarrow low melting gel (Nuscreen)

4 PCR for CHO clone did not work
repeat PCR

SUPERVISOR

DATE 08/31/95

9/4/95 PCR to produce BamHI fragment for TNFR

Φ extract 2x

info tag

cells ext

extract ppt



I cut - check 12 on gel

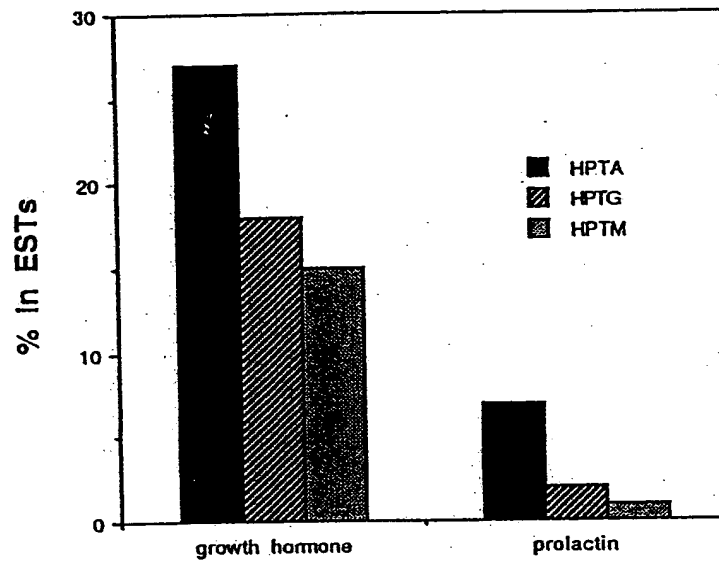
give to Lily for clone into

CHO vectors

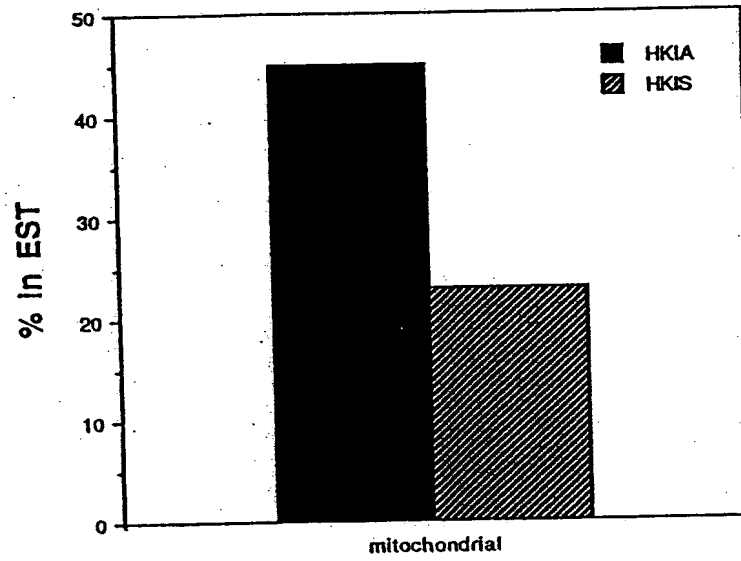
9/6/95 Summary on subtraction using biotinylated drivers generated by PCR using b2a.c4 dcrp

	Driver	PRL	G4	mito
HPTA	—	6.5%	21%	—
HPTG	G4 PL	1.6%	18%	—
HPTM	G4 PL	1.2%	15%	—
HPDB	—			34%
HSDS	mito			28%
HKIA	—			45%
HKIS	mito			23%

Subtraction result



Subtraction



9/6/95 modify the approach:

① using regulator drop to generate ss DNA

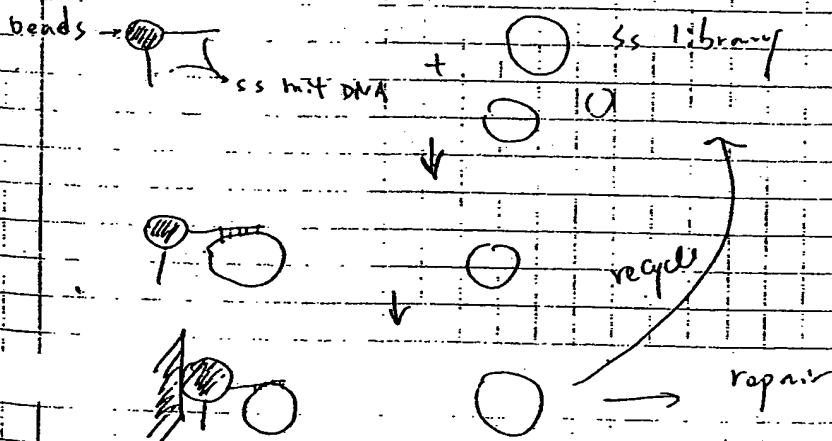
② photo biotin DNA

this is proven to be efficient

③ Try both long hybridization at 42°C and short hybridization at RT 1 hr

④ remove biotin by extract add one more step showed no difference by using magnetic beads

9/5 Discussion w/ Fouad idea



P.F. 202412-72

NORTHERN BLOT DATA SHEET

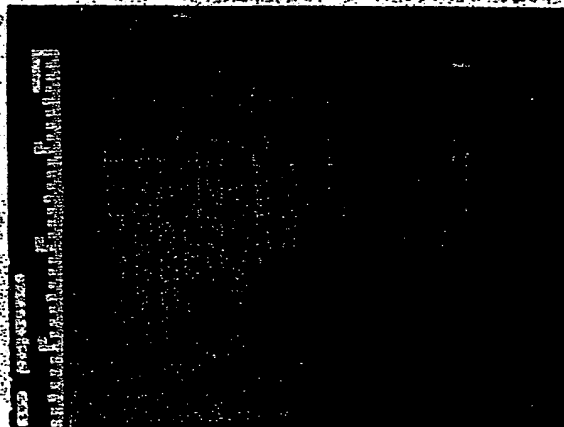
OPERATOR: Lily Xing

DATE 9/1/94

LANE #	NAME	RNA (μ l/10 μ g)	Note
1	Brain	20 μ l	
2	kidney	"	
3	small intestine	"	
4	testis	"	
5	pancreas	"	
6	prostate	"	
7	Heart	"	
8	Liver	"	
9	lung	"	
10	thymus	"	
11	spleen	"	
12	placenta	"	
13	Colon	"	
14	ovary	"	
15	leukocytes	"	
16	muscle	"	
17			
18			
19			
20			

NOTE:

#3 gel



NORTHERN BLOT DATA SHEET

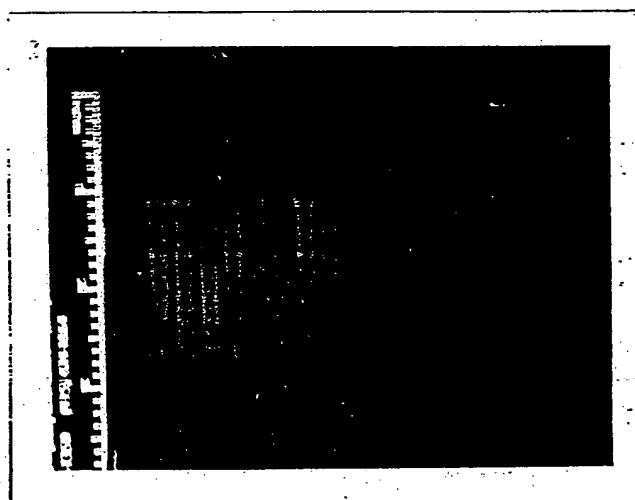
OPERATOR: Lily Xing

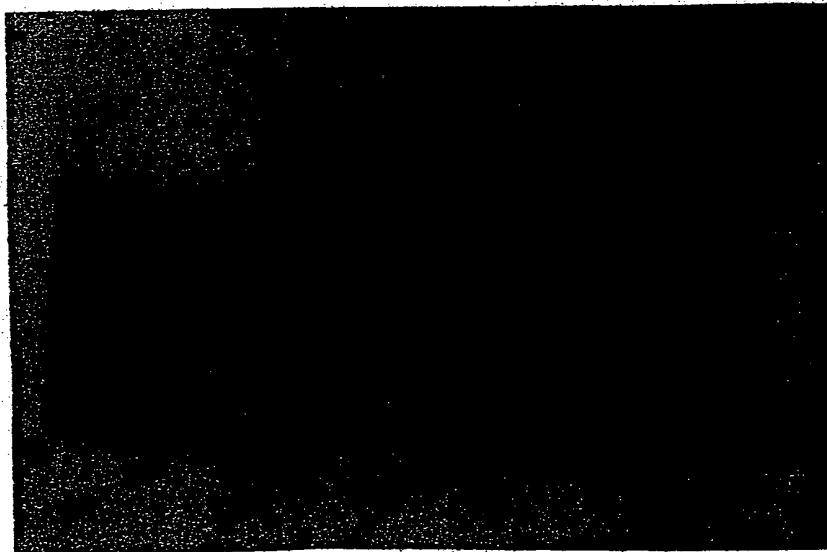
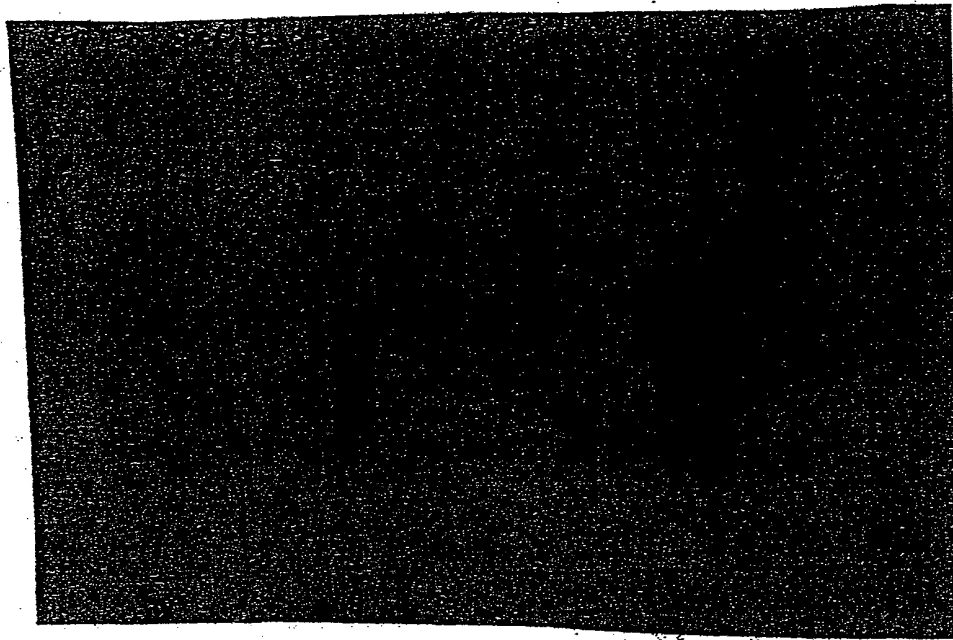
DATE 9/1/94

LANE #	NAME	RNA (μ l/10 μ g)	Note
1	Brain	20 μ g	
2	Kidney	"	
3	Small intestine	"	
4	Testis	"	
5	Pancreas	"	
6	Prostate	"	
7	Heart	"	
8	Liver	"	
9	Lung	"	
10	Thymus	"	
11	Spleen	"	
12	Placenta	"	
13	Colon	"	
14	Ovary	"	
15	Leukocytes	"	
16	Muscle	"	
17			
18			
19			
20			

NOTE:

#3 gel





9/18/95 Design oligos for SOD4 to determine which ATG is the real ATG

3 oligos BAAATTAACCTCACTAAAGGACCATCATG GGCAGCGGCCAA
T₃ - SOD ATG

SOD ATG₂ _____ ATG G TCTTGATACAC

SOD ATG₃ _____ ATGACCTGTCAGAGC

PCR to generate PCR product for T₃T

3' olig SOD EAD

CGTCTAGAGGTCTGCTCAAA GGTGGG



SOD T₃ + T₇ PCR



9/19 Subtraction Result

Sequence of two new HPT subtracted library come back
in HPTX which is long hyb (0.2 at 42°C)

GH reduced to 10% protection to 0%

HPTX — short hyb is not as good

GH → 15% protection 3%

→ try hybridization with 5% PEG

9/20/95 TNT

promega kit

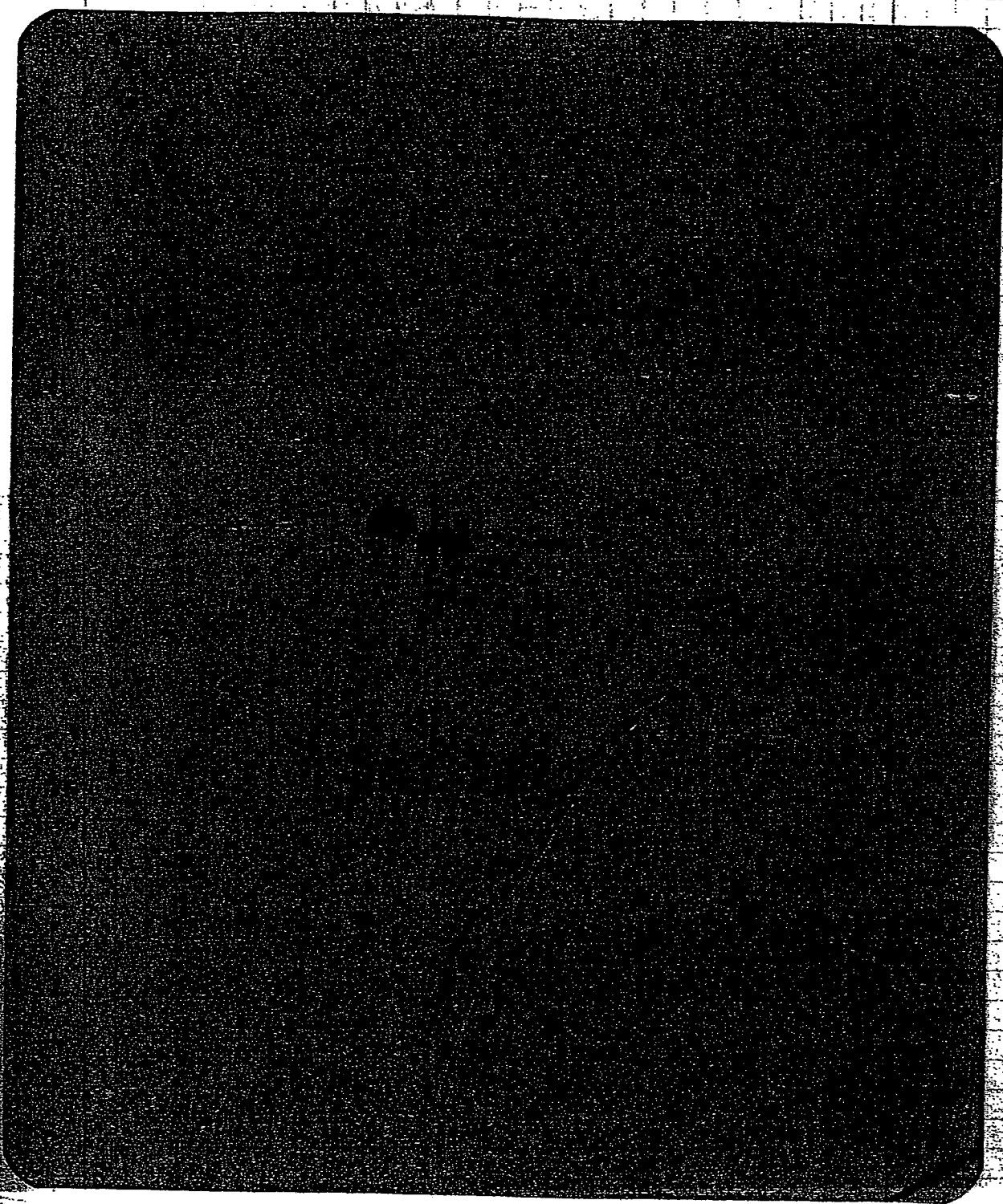
DNA: pBluescript sk
500 full length in pBluescript
PCR product from 8161
8162
8163

T₇-CsGib in P₄Z

make a premix

{ 12.5 ml Rabbit Reti-cubate Lyse
0.1 ml bt
0.5 ml T₇ or T₇ RNA polymerase
0.5 ml Am¹²⁵ Acid - met
2 ml 35S - met
0.5 λ RNA inhibitor from Bolygen
3 λ DNA
8 λ ddH₂O

30°C 1 hr



9/25 repeat TNT

10x reaction
 2nd PCR product similar
 amount

Full length	SDS		
ATG1	-	1	27 Kd
ATG2	-	2	24 Kd
ATG3	-	3	21 Kd

30°C 1 hr

add 10x loading dye boil for 2 min
 Load 10x on 10% SDS gel

This experiment
 indicates there is
 another ATG upstream
 maybe the real ATG
 check seq. if
 there is another
 19 AA upstream
 this will move
 the position of

SUPERVISOR

DATE

09/27/93

10/4/95

7
27 Kd
24 Kd
21 Kd

Subtraction result came back with a nice improvement
by adding 5% PEG (P200) in hybridization mix. it may be increased
hybridization efficiency

result:	before subtraction:	GH	pr
		27%	7%
	after subtraction:	5%	1%

— clone Full length TGF α by PCR HPD 1.6kb

HPD was mass excised and used to PCR using

T₁₃ Reverse + HLTB771Fp06
+ HLTB771Fp04

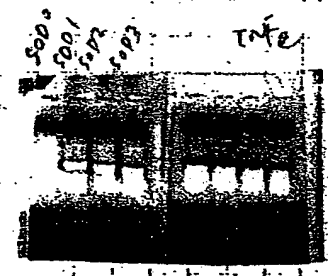
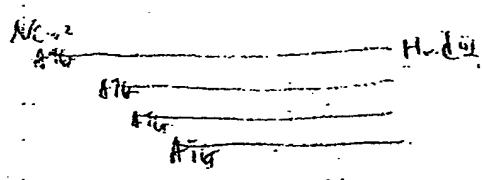
— pure band of 0.8 kb seen

— Second PCR

1) first PCR

T₃ + HLTB771Fp05
Fp06

— PCR to construct SOD4
expression vectors



— Lily will clone into 70560

10/5/85

Gene traps

genes: TNFR p55
 TNFS
 TGFP — WWH
 Rad16 — YFW

labeled oligos: w/ TDT

TGFP 11362
 11356

TNFS TNFS Rpo1

TNFR p55 cap1
 +
 Rpo2

Rad16 - R8
 +
 R11

Coding and working

produce SS DNA by gene T EST

Chivspont library

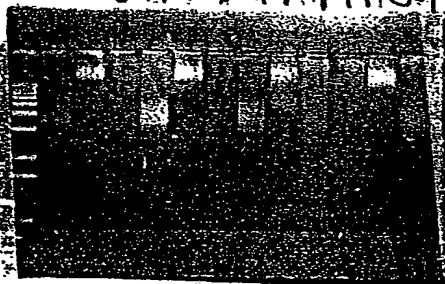
Leukocyt

Leuk X
 Gen 4
 Gen 8

Leukocyt

Brain

Leuk
 Leuk
 Brain



TNFS → Leuk

TGFP → m.w.

Rad16 → Leuk

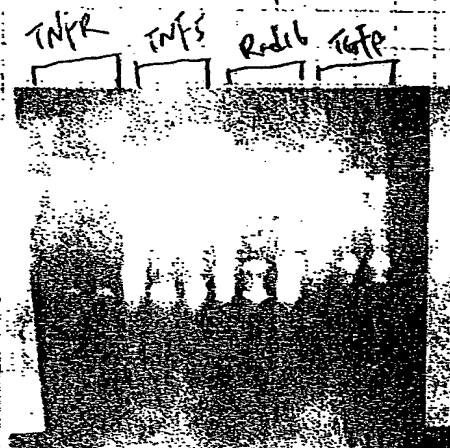
TNFR p55

10/6/95 Repeat biotin labeling of oligos

ethanol ppt oligos final concentration 200 ng/μl

3/18 add (12 μl)

10 μl 5x TdT bfr
5 μl biotin-CTP-dep
5 μl TdT



10/9/95 capture

add 6 μl 4x bfr Δ 95°C 1'

add 5 μl TNFR oligo to Brain

0.5 μl other oligos to Leukocyte - TNFS

Leukocyte - Rad66

Mix - TGFP

Hyb:

37°C 1 hr

treat 5A - Magnetic beads, capture, wash

repair all 10 μl

10/9/95

transfer to DH10B from BRL

plate

10 λ 100 λ

TNFRp55 —

40 colony

TNFS —

41

TGFP —

1

RAD 16 —

6

add 1 ml 2x freeze buffer to remaining

10/10/95 PCR to identify positive clones.

2 gene specific primers

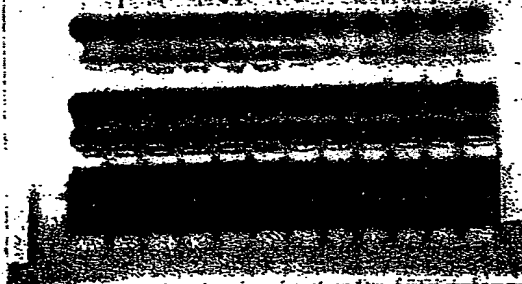
TNFS



5% clones are positive

2 gene specific primers

TNFRp55



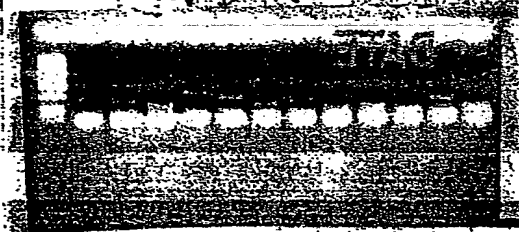
~5% clones positive



not so colony hybrid

Show only 32/1000
hybridize

GAP + TNFS/EP1



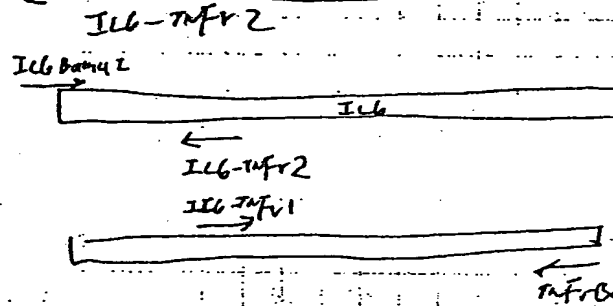
10/16/95 Fusion construct for TNF α with IL6 signal

PCR:

oligos: IL6 BamHI

C G C G G A T C C A T G A A C C A T G A A C T C C T T C T C C A C
Met

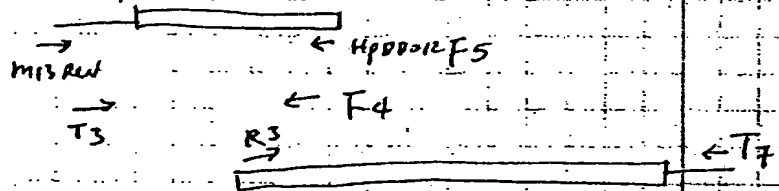
IL6-TNF α 1 IL6 TNF α
C G C G G A T C C A T G A A C C A T G A A C T C C T T C T C C A C



50 ul reaction 58 program

Fusion for Full length TNF α (HPD012)

PCR from HPD library



SUPERVISOR

DATE 10/17/95

Signature

10/23 seq analysis of 4 HTBN61 clones

HTBN61 508 — wrong clone

HTBN61 523 — wrong clone

HTBN61 502 — wrong clone

HTBN60 507 — wrong clone

design new primers for oligo capture?

have L ly in a colony hybridization

the construct of IL6/TNF α is missing kozak sequence

new oligo is made IL6's'

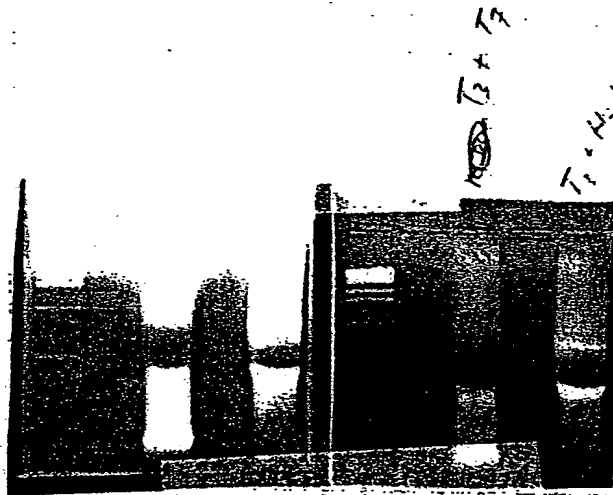
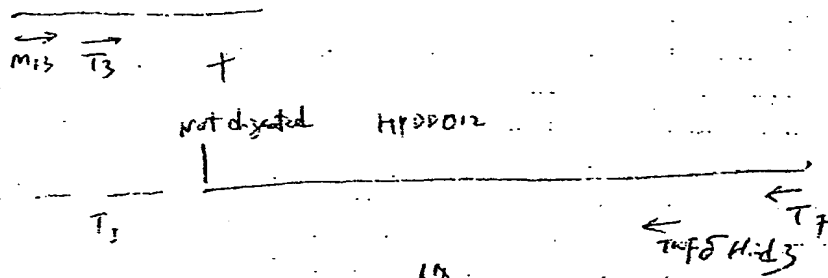
GCG GGATCC GCGGCC ATG TCC TTC TCC GC
BamHI kozak met

PCR to generate IL6/TNF α fusion

clones are made into the two CHO vectors by 21/1/97

10/26 still having problem get HpaD912 PCR fragment

PCR products



last melting gel
Φ 2x
CHCl₃

1 kb
0.6 kb

digest w/ Hind3 + BamHI

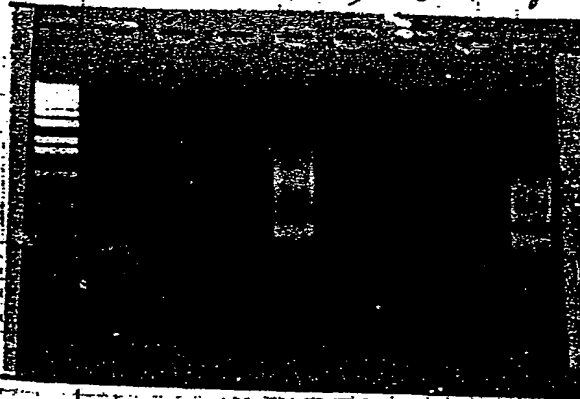
Clone in pbluescript HpaD912 + BamHI

primer template

10/26

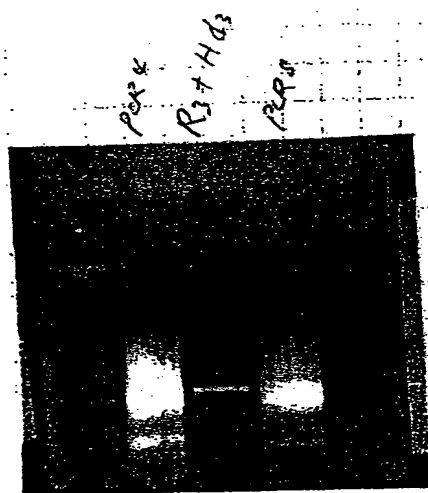
PCR products 5 μl/50

1 2 3 4 5 6 7 8



- | | | | | |
|---|--------------|-----------|-----------|---------|
| 1 | T3 + F2 | } HpaD912 | - PCR Ⓢ - | HpaD912 |
| 2 | T7 + R3 | | | |
| 3 | T7 + F2 + R3 | | | |
| 4 | T3 + F2 | } HpaD | - PCR Ⓢ - | HpaD |
| 5 | T3 + F2 | | | |
| 6 | T7 + R3 | | | |
| 7 | T7 + F2 + R3 | - PCR Ⓢ - | HpaD | |
| 8 | T3 + F2 | | | |

10/17 low melting gel



cut out DNA

PCR4 → 0.6-1.1 kb

PCR8 -

R3+Hd3 →

(PCR7)

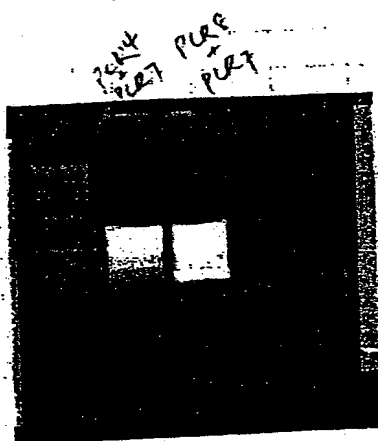
Φ 2x

cut, 1x

extract. p₁⁺

mix PCR4 + PCR7
PCR8 + PCR7

PCR using T3 + Hd3



low melting gel purify top band

HindIII + BamHI digestion

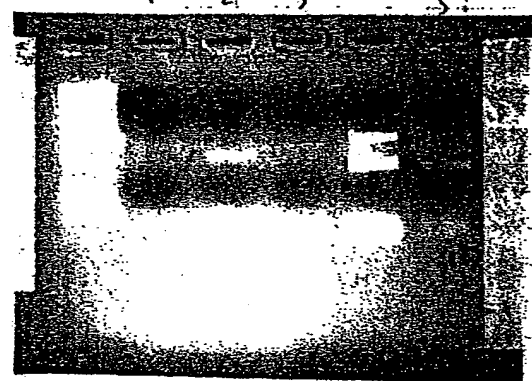
clone into pBluescript HindIII + BamHI digestion

PCR check → no clone found

11/7/95
orig

flanking Tnfo Rpo7 + Rpo7

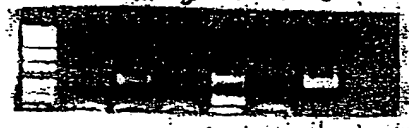
PCR	DNA	primer
①	HPD 1.6m	Rpo7 + Fpo7
②	HPD 1.6m	Rpo7 + Fpo7 + Tnfo Bam + Tnfo H-d
③	HPD 1.6m	Tnfo Bam + H-d
④	HUTB7159	Rpo7 + Fpo7 $\xrightarrow{\text{expect}}$ 1.7 kb
⑤	HUTB7159	Bam + H-d $\xrightarrow{\text{expect}}$ 600 bp



wrong size for 2 bands products

12/10 New primer made for Tnfo Bam

PCR	DNA	primer
①	HPD 1.6m	Rpo7 + Fpo7
②	HPD 1.6m	Bam + H-d
③	PCR ①	Rpo7 + Fpo7
④	PCR ①	Bam + H-d
⑤	HUTB7159	Rpo7 + Fpo7
⑥	HUTB7159	Bam + H-d



140

11/11/95 2% can melting gel purification PUR 2 & PCR C

Φ1 Φ1000z endr exhaust ppt

digest with BamHI + H-d

also digest Vector pOE-9

Ligation on

Design oligos to test ligation for SAGE

Ligation oligo 1 GAGTCAGTTCATG CCAACGGCATG

Ligation oligo 2 CCGTTTGGCATTG AACTGACT CCATC

SUPERVISOR-

DATE-

11-20-95

Patricia Dillon

11/20/95 RACE for HTBN61 TNFRp55 homologs

The following library has the gene based on PCR using 2 gene specific primers

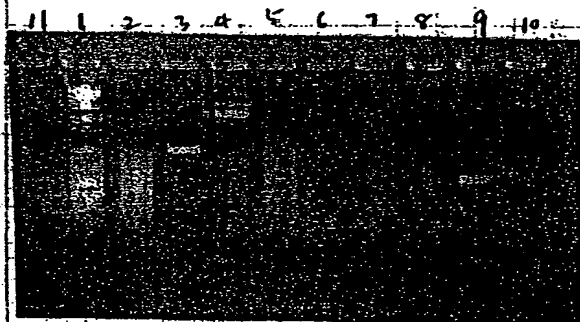
HCO HLO HFV HFB HPD HAP HTX HLE9
1 2 3 4 5 6 7 8

M13RV T3

← F3 ← F4

PCR using M13RV + F4

9 = HPD
TNFRp55 + Fp07
10 : RpoE + Fp06
11 : RpoB + 5HindIII



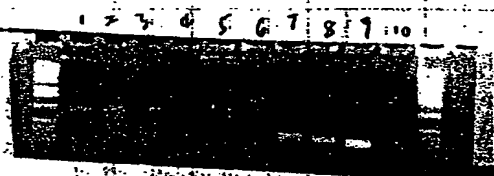
Second PCR

T3 + F3

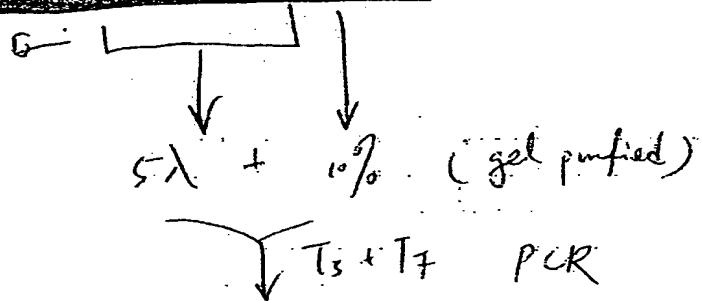
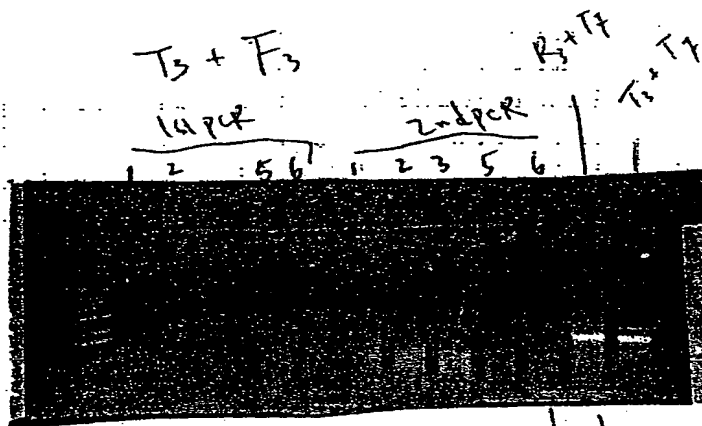
1-8 template PCR 1-8

9 HTBN61

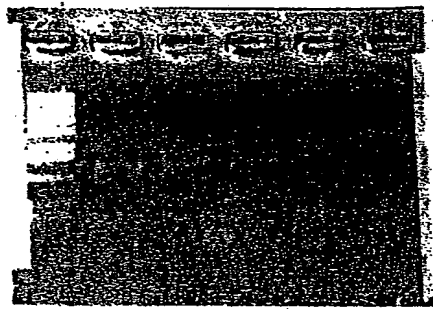
10 HTBN61 T7 + Rpo1



11/21/95



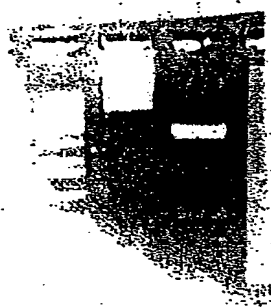
11/28



no specific products

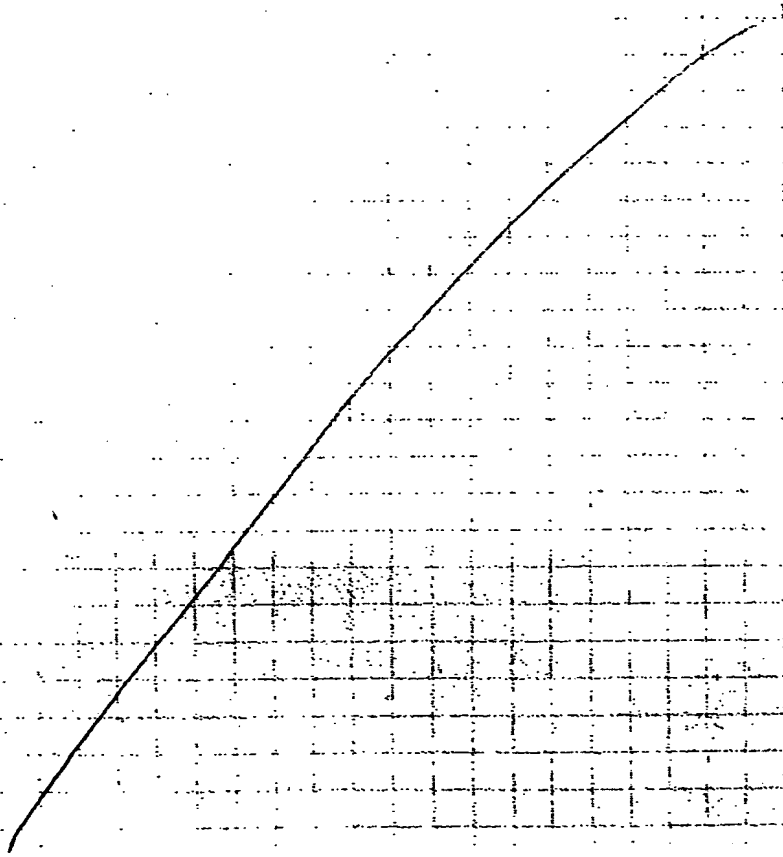
11/28 Trf 5 His tag construct

Seq verified digestion w/ Bam + Hind III



Signed by R.G. and K.R.

gave DNA to protein expression



12/6/95 prepare linkers for SAGE

large scale oligo synthesis each 7.5 μ g

linker A

TTTTAATTAACCTCACTAAAGGGCTCGCACGGATGCATG 4368
 TTAATTGGGAGTGATTTCCTCCGAGCGTGCCTAC 4370

linker B

TTTGTGAATACGACTCACTATAGGGCAAGTCGGATGCATG 4369
 CATTATGCTGAGTGATATCCCGTTCAGCCTAC 4371

12% urea acrylamide gel purify the oligos
 put through C18 column

or ϕ /C18 extr ethanol ppt + equal vol 1M Tris pH 7.5
 3.5 vol 100% EtOH

Concentration

Sample	abs	abs		260.0 nm	260.0 nm
11	260.0 nm	280.0 nm		260.0 nm	260.0 nm
4368	0.3014	0.1508	4.5 v/v	1.5797	0.6330
2	0.3548	0.2061	5.3	1.7045	0.5367
3	0.3056	0.1275	4.5	1.5468	0.6465
4	0.3139	0.2102	4.5	1.5173	0.5591
5	0.0782	0.0489	1.1	1.5531	0.6414
6	0.0708	0.0456	1.2	1.7304	0.5773
7	0.1140	0.0757	1.7	1.5114	0.6616
3	0.1608	0.0650	1.5	1.5292	0.6539
3					

 ϕ extracted

gel purified

Anneal

80 μ g (4368) + 64 μ g (4370) + 20 μ l 10x kinase buffer80 μ g (4369) + 64 μ g (4371)

70 mM Tris-HCl

10 mM MgCl₂

1 mM DTT

add H₂O to 200 μ l

A B gel purified
A' B' ϕ 100₃/chool μ T

65°C → cool to 4°C put heat block on bench

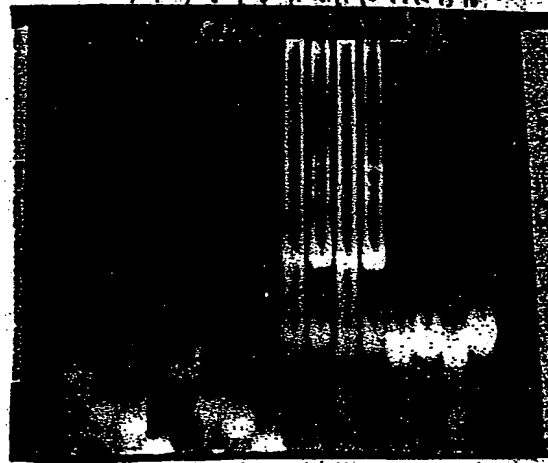
add 1 λ 100 mm A-T-P
1 λ 100 mm ddATP
2 λ P-N-K
2 λ Klenow

37°C 1 hr

take 2 λ each ligate in 10 λ 2 λ S-L BRC ligation buffer
1 λ NEB high conc ligase

RT 2-3 hrs

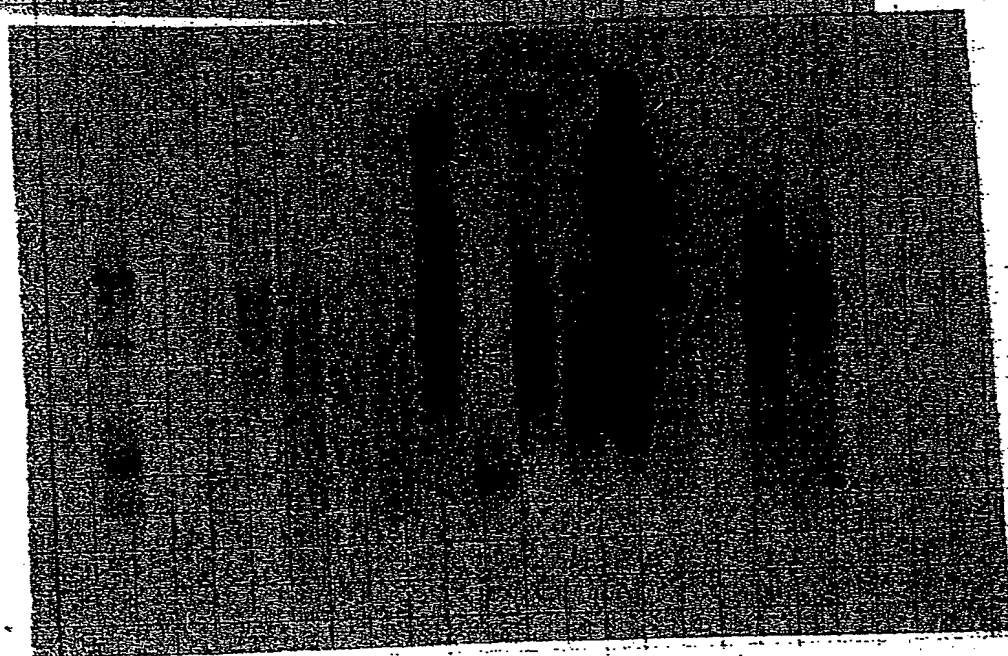
12% native agarose gel



1	4368	} ϕ 100 ₃ phage
2	4370	
3	4369	
4	4371	
5	4368	} gel purified
6	4370	
7	4369	
8	4371	
9	Linker A	} Self-ligation
10	Linker A'	
11	B	
12	B'	
13	Linker A	
14	A'	
15	B	
16	B'	

12/12/95 Northern form HTIBal61 TAFR

1 2 3 4 5 6 7 8 9 10 11 12 13
 14. Kidney

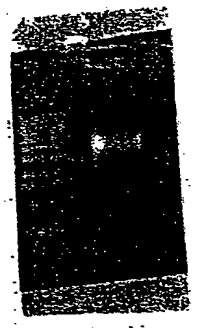


12/11/95 SAGE
Linkers A and Linkers B

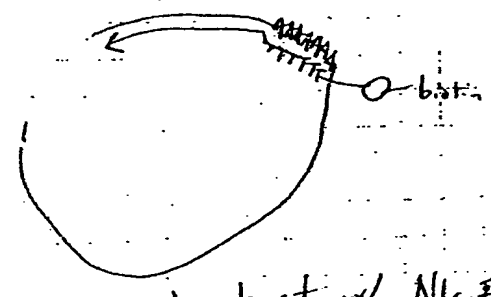
13
Gallballe
new

	100	200	300	400	500
12.00X					
14.00X					
16.00X					
18.00X					

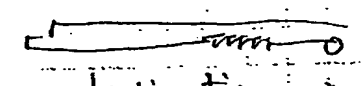
HBC library plasmid DNA digest w/ XhoI
total 7 μ g



take $\frac{1}{2}$ (3 μ g)
 \downarrow 96°C 5 min
 add 0.5 μ g biotinylated oligo dT (NEB)
 \downarrow 37°C
 Klenow 1 μ l 100 mM dH₂O
 30 min



\downarrow digest w/ NlaIII



\downarrow ligation in 20 μ l PCR buffer
 RT 3 hr
 Linker A 0.2 μ g
 Linker B 1.2 μ g

12/12 prewash streptavidin magnetic beads

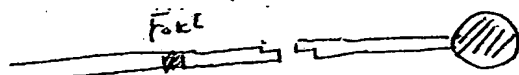
TE wash 3X

resuspend in 30 λ TE add ligation

bind 1 hr at RT with occasional

wash w/ TE/1m NaCl 2X transfer to new tube
wash 2X more

digestion with FokI at 37°C



Φ /C19s et al. pTV T4 DNA pol/uvase

+ 1 λ 100mM dTP

RT 30'

↓ Ligation

8°C

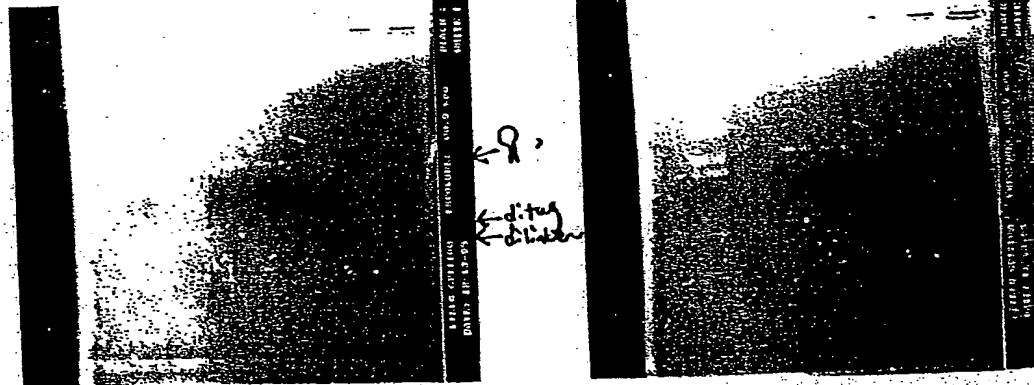
mix A + B

0.1 λ

↓ PCR T3 + T7 66 program

0.1 1. 4 λ ligation as template (30 cycles)

0.1 λ ↓



12/12 prewash streptavidin magnetic beads

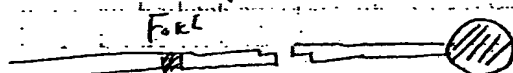
TE wash 3X

resuspend in 30 λ TE add ligation

bind 1 hr at RT mix occasionally

wash w/ TE/1m NaCl 2X, transfer to new tube
wash 2X more

digestion with FokI at 37°C



Φ /Cts shad pTV T4 DNA pol/hovase

+ 1 λ 100mM dATP

RT 30'

↓ Ligation

8°C

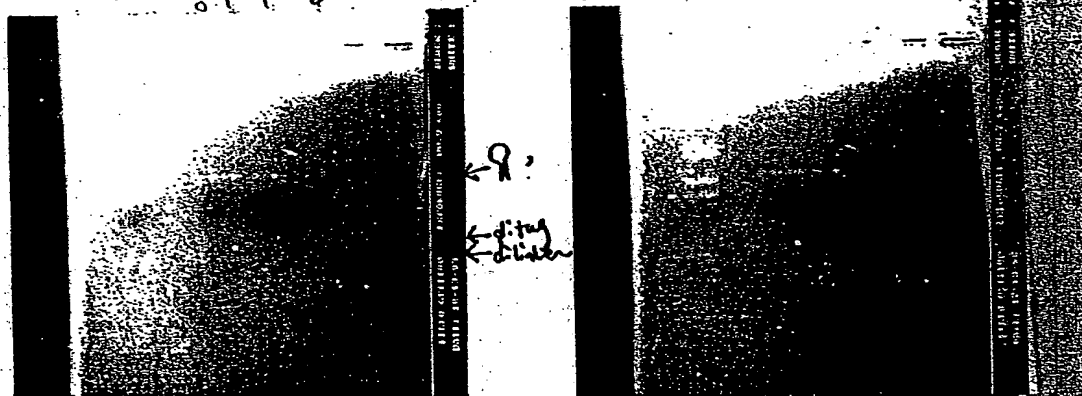
mix A + B

o/n

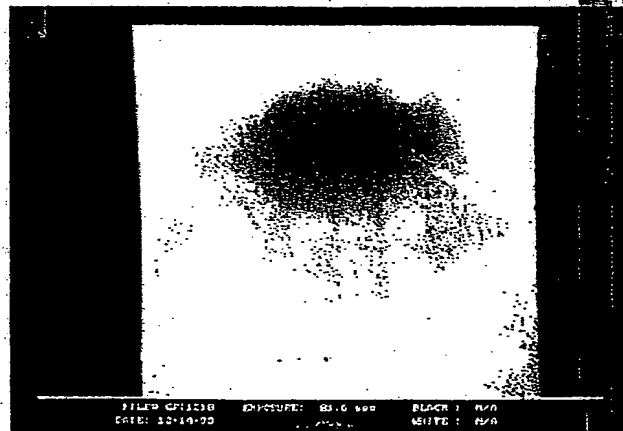
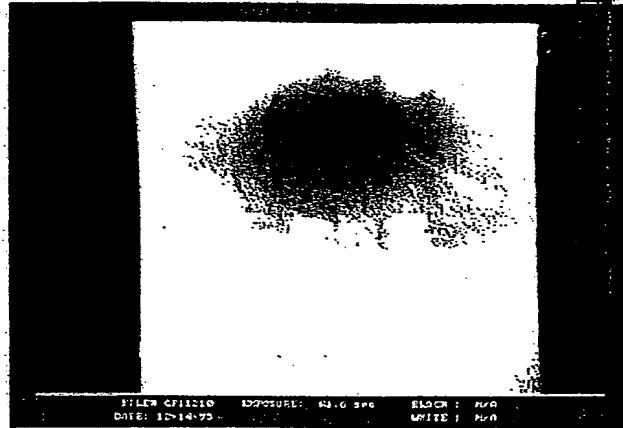
↓ PCR T3 + T7 66 program

o.l. 1. 4 λ ligation as template (30 cycles)

o.l. 1. +



5c



FILED 0711210 00000001 00.0 000
DATE: 12-14-73 WHITE : 000

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.